

SEQUENCE LISTING

SUMMARY OF SEQUENCES

SEQ ID NO: 1 is the N-terminal amino acid sequence for the YKL-40 protein.

SEQ ID NO: 2 is an internal amino acid sequence of the YKL-40 protein ("YKL-40 Peptide A").

SEQ ID NO: 3 is another internal amino acid sequence of the YKL-40 protein ("YKL-30 Peptide B").

SEQ ID NO: 4 is the cDNA nucleotide sequence for the coding region of the gene for YKL-40. The initiation codon for the mature, secreted protein begins at nucleotide 135.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
- (ii) TITLE OF INVENTION: ASSAY FOR YKL-40 AS A MARKER FOR
DEGRADATION OF MAMMALIAN CONNECTIVE TISSUE MATRICES
- (iii) NUMBER OF SEQUENCES: 4
- 10 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: SPENSLEY HORN JUBAS & LUBITZ
(B) STREET: 1880 CENTURY PARK EAST, FIFTH FLOOR
(C) CITY: LOS ANGELES
(D) STATE: CALIFORNIA
(E) COUNTRY: USA
15 (F) ZIP: 90067
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
20 (D) SOFTWARE: Patent In Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: PCT
(B) FILING DATE: 08-JUL-1994
(C) CLASSIFICATION:
- 25 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: HOWELLS, STACY L.
(B) REGISTRATION NUMBER: 34,842
(C) REFERENCE/DOCKET NUMBER: FD 3665
- (ix) TELECOMMUNICATION INFORMATION:
30 (A) TELEPHONE: 619/455-5100
(B) TELEFAX: 619/455-5110

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
35 (A) LENGTH: 25 amino acids
(B) TYPE: amino acid

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(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: YKL-40 N-TERMINAL SEQUENCE

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Tyr Lys Leu Val Cys Tyr Tyr Thr Ser Trp Ser Gln Tyr Arg Glu Gly
1 5 10 15

Asp Gly Ser Xaa Phe Pro Asp Ala Leu
20 25

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(B) CLONE: YKL-40 INTERNAL PEPTIDE A

(ix) FEATURE:

(A) NAME/KEY: Peptide

(B) LOCATION: 1..19

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Leu Asn Thr Leu Lys Asn Arg Asn Pro Asn Leu Lys Thr Leu Leu Ser
1 5 10 15

Val Gly Gly

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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (B) CLONE: YKL-40 INTERNAL PEPTIDE B

(ix) FEATURE:

- (A) NAME/KEY: Peptide
- (B) LOCATION: 1..7

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu Arg Leu Gly Ala Pro Ala
1 5

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1681 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vii) IMMEDIATE SOURCE:

- (B) CLONE: YKL-40

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 135..1681

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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CTAGGTAGCT GGCACCAGGA GCCGTGGGCA AGGGAAGAGG CCACACCCTG CCCTGCTCTG 60
CTGCAGCCAG AATGGGTGTG AAGGCGTCTC AAACAGGCTT TGTGGTCCTG GTGCTGCTCC 120
AGTGCTGCTC TGCATACAAA CTGCTCTGCT ACTACACCAG CTGGTCCCAG TACCGGGAAG 180
GCGATGGGAG CTGCTTCCCA GATGCCCTTG ACCGCTTCCT GTGTACCCAC ATCATCTACA 240
5 GCTTTGCCAA TATAAGCAAC GATCAGATCG ACACCTGGGA GTGGAATGAT GTGACGCTCT 300
ACGGCATGCT CAACACACTC AACAAACAGA ACCCCAACCT GAAGACTCTC TTGTCTGTCTG 360
GAGGATGGAA CTTTGGGTCT CAAAGATTTT CCAAGATAGC CTCCAACACC CAGAGTCGCC 420
GGACTTTCAT CAAGTCAGTA CCGCCATTTC TCGGCACCCA TGGCTTTGAT GGGCGTGACC 480
TTGCCTGGCT CTACCCTGGA CGGAGAGACA AACACCATT TACCACCCTA ATCAAGGAAA 540
10 TGAAGGCCGA ATTTATAAAG GAAGCCCAGC CAGGGAAAAA GCAGCTCCTG CTCAGCGCAG 600
CACTGTCTGC GGGGAAGGTC ACCATTGACA GCAGCTATGA CATTGCCAAG ATATCCCAAC 660
ACCTGGATTT CATTAGCATC ATGACCTACG ATTTTCATGG CGCCTGGCGT GGGACCACAG 720
GCCATCACAG TCCCCTGTTC CGAGGTCAGG AGGATGCAAG TCCTGACAGA TTCAGCAACA 780
CTGACTATGC TGTGGGGTAC ATGTTGAGGC TGGGGGCTCC TGCCAGTAAG CTGGTGATGG 840
15 GCATCCCCAC CTTCCGGGAGG AGCTTCACTC TGGCTTCTTC TGAGACTGGT GTTCCAGCGC 900
CAATCTCAGG ACCGGGAATT CCAGGCCGGT TCACCAAGGA GGCAGGGACC CTTGCCTACT 960
ATGAGATCTG TGACTTCCTC CGCGGAGCCA CAGTCCATAG AACCTCGGC CAGCAGGTCC 1020
CCTATGCCAC CAAGGGCAAC CAGTGGGTAG GATACGACGA CCAGGAAAGC GTCAAAAGCA 1080
AGGTGCAGTA CCTGAAGGAT AGGCAGCTGG CAGGCGCCAT GGTATGGGCC CTGGACCTGG 1140
20 ATGACTTCCA GGGCTCCTTC TGCGGCCAGG ATCTGCGCTT CCCTCTCACC AATGCCATCA 1200
AGGATGCACT CGCTGCAACG TAGCCCTCTG TTCTGCACAC AGCACGGGGG CCAAGGATGC 1260
CCCGTCCCCG TCTGGCTGGC CGGGAGCCTG ATCACCTGCC CTGCTGAGTC CCAGGCTGAG 1320
CCTCAGTCTC CCTCCCTTGG GGCCTATGCA GAGGTCCACA ACACACAGAT TTGAGCTCAG 1380

CCCTGGTGGG CAGAGAGGTA CACACTGTGTT GATGATTAAT GGAAATGTTT ACAGATCCCC 1440
AAGCCTGGCA AGGGAATTTC TTCAACTTSC TGCCCCCTAG CCCTCCTTAT CAAAGGACAC 1500
CATTTTGGCA AGCTCTATCA CCAAGGAGCC AAACATCCTA CAAGACACAG TGACCATACT 1560
AATTATACCC CCTGCAAAGC CAC TTGAAA CCTTCACTTA GGAACGTAAT CGTGTCCCCCT 1620
5 ATCCTACTTC CCCTTCCTAA TTCCACAGCT GGTCAATAAA GTACAAGAGT TTAACAGTGT 1680
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